Abstract

Disclosed is a method for distinguishing AML subtypes with recurring genetic aberrations t(8;21), t(15;17), t(11q23)/MLL, inv(3)/t(3;3), inv(16), AML_komplext , trisomy 8 sole, trisomy 11 sole, trisomy 13 sole, monosomy 7 sole, del(5q) and/or del(9q) in a sample by determining the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.